

GenCore version 5.1.3  
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OW protein - protein search, using sw model

Run on: December 19, 2002, 14:50:37 ; Search time 14 Seconds

(without alignments)  
1682.754 Million cell updates/sec

Title: US-08-813-323b-2

Perfect score: 3008  
Sequence: 1 MESSKKMDSPGALQTNPLK.....IKDDTFIKIVDTSDLPDP 568

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query %	Match Length	ID	Description
1	3008	100.0	568	1 TRA3_HUMAN	Q13114 homo sapien
2	2886.5	96.0	567	1 TRA3_MOUSE	Q60803 mus musculu
3	837.5	27.8	501	1 TRA2_MOUSE	P39429 mus musculu
4	744	24.7	501	1 TRA2_HUMAN	Q12933 homo sapien
5	636.5	21.2	416	1 TRA1_HUMAN	Q13077 homo sapien
6	628	20.9	409	1 TRA1_MOUSE	P39428 mus musculu
7	201	6.7	458	1 DGI7_MOUSE	P11467 dictyostell
8	159	5.3	634	1 D147_MOUSE	Q61510 mus musculu
9	151.5	5.0	704	1 MEPR_MOUSE	Q61847 mus musculu
10	150	5.0	1005	1 RA50_MOUSE	Q58718 methanococ
11	149.5	5.0	919	1 RA50_MOUSE	Q9YF21 aeropyrum p
12	148.5	4.9	1816	1 LMA4_MOUSE	P97927 mus musculu
13	148	4.9	1957	1 YD86_MOUSE	Q10411 schizosacch
14	146.5	4.9	2230	1 GOG4_HUMAN	Q13439 homo sapien
15	146	4.9	1102	1 MYSC_CHICK	P29616 gallus gall
16	145	4.8	1679	1 YIO9_YEAST	P40457 saccharomyc
17	144.5	4.8	1104	1 NEX1_HUMAN	Q12985 homo sapien
18	144	4.8	1727	1 ALM1_MOUSE	Q9UK5 schizosacch
19	143.5	4.8	551	1 RN27_MOUSE	Q99P12 mus musculu
20	143.5	4.8	852	1 RA50_MOUSE	Q9X1X1 thermotoga
21	143.5	4.8	3210	1 CENF_HUMAN	P49454 homo sapien
22	141	4.7	879	1 RA50_MOUSE	Q58687 pyrococcus
23	141	4.7	1046	1 SBCC_MOUSE	Q9CF0 lactococcus
24	141	4.7	1940	1 MYH3_MOUSE	P12847 rattus norv
25	140.5	4.7	425	1 TRM3_HUMAN	Q9BZ9 homo sapien
26	140.5	4.7	999	1 CARE_MOUSE	Q9BZ9 mus musculu
27	140	4.7	551	1 RN27_HUMAN	Q9BZ9 mus musculu
28	139.5	4.6	794	1 HMMR_MOUSE	Q00547 mus musculu
29	139	4.6	390	1 TET1_BOVIN	P27628 bos taurus
30	138	4.6	624	1 A33_MOUSE	Q02084 plasmodesm
31	137.5	4.6	1607	1 MIPR_MOUSE	Q25410 lymnaea sta
32	137	4.6	495	1 RA18_HUMAN	Q9NS91 homo sapien
33	137	4.6	886	1 RA50_MOUSE	Q29230 archaeglob

34	137	4.6	886	1 RA50_MOUSE	Q03600 sulfobus
35	137	4.6	1938	1 MYH3_HUMAN	Q9UKX3 homo sapien
36	137	4.6	1940	1 MYH3_HUMAN	P11055 homo sapien
37	136.5	4.5	944	1 MYH3_MOUSE	P37380 saccharomyc
38	136	4.5	704	1 MEPR_MOUSE	P28826 rattus norv
39	135.5	4.5	1941	1 MYH2_HUMAN	Q9UKX2 homo sapien
40	135	4.5	1939	1 MYH1_HUMAN	P12882 homo sapien
41	134.5	4.5	1012	1 CX05_HUMAN	O75665 homo sapien
42	134	4.5	1940	1 MYH3_CHICK	P02565 gallus gall
43	132.5	4.4	630	1 Z147_HUMAN	Q14258 homo sapien
44	132	4.4	747	1 MEPR_MOUSE	P28825 mus musculu
45	132	4.4	1084	1 MYSS_MOUSE	P02562 oryctolagus

## ALIGNMENTS

RESULT 1  
ID TRA3\_HUMAN STANDARD: PRT; 568 AA.  
AC Q13114: Q13076: Q13947: Q12990:  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE TNF receptor associated factor 3 (CD40 receptor associated factor 1)  
DE (CD40) (CD40 binding protein) (CD40BP) (LMP1 associated protein)  
DE (LAP1) (CAP-1).  
GN TRAF3 OR CRF1 OR CAP1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95184010; PubMed=7533327;  
RA Cheng G., Cleary A.M., Ye Z.S., Hong D.I., Lederman S., Baltimore D.,  
RT "Involvement of CRF1, a relative of TRAF, in CD40 signaling.";  
RL Science 267:1494-1498(1995).  
RN [2]  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RC TISSUE=Lymphoma;  
RX MEDLINE=95163092; PubMed=7859281;  
RA Mosialos G., Birkenbach M., Yalamanchili R., VanArsdale T., Ware C.,  
RT Kleef E.;  
RL "The Epstein-Barr virus transforming protein LMP1 engages signaling  
RT proteins for the tumor necrosis factor receptor family.";  
RN Cell 80:389-399(1995).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fetal brain;  
RX MEDLINE=95129692; PubMed=7530216;  
RA Sato T., Irie S., Reed J.C.;  
RT "A novel member of the TRAF family of putative signal transducing  
RT proteins binds to the cytosolic domain of CD40.";  
RN FEBS Lett. 358:113-118(1995).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95073988; PubMed=7527023;  
RA Hu H.M., O'Rourke K., Boguski M.S., Dixit V.M.;  
RT "A novel RING finger protein interacts with the cytoplasmic domain of  
RT CD40.";  
RL J. Biol. Chem. 269:30069-30072(1994).  
CC - FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN  
CC OF THE 75 KDA TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2). ALSO BINDS  
CC TO CD40 AND THE LYMPHOTOXIN-BETA RECEPTOR.  
CC - SUBUNIT: HOMODIMER OR HETERODIMER WITH OTHER TNF RECEPTOR  
CC ASSOCIATED FACTORS (POTENTIAL).  
CC - SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
CC - SIMILARITY: CONTAINS 1 MATH/TRAF DOMAIN.  
CC - SIMILARITY: CONTAINS 2 TRAF-TYPE ZINC FINGERS.  
CC  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

QY	1	MESSKKMDSPALQTNPEPLKLTHTDRSAGTPVFEVDEOGYKKEKFKYKTEADKXCEKCHLYL	60
Db	1	MESSKKMDSPALQTNPEPLKLTHTDRSAGTPVFEVDEOGYKKEKFKYKTEADKXCEKCHLYL	60
QY	61	CSPKOTEGCHFFCSGCMALLSSSSPKCTAOQESTYVKRKYKMDCKREKELLATQYCNNE	120
Db	61	CSPKOTEGCHFFCSGCMALLSSSSPKCTAOQESTYVKRKYKMDCKREKELLATQYCNNE	120
QY	121	SRGCAEQLTLGHLVHLKNDCHFELPCVRPDCKEKYLKRDLRHVEKACKYREATCSHC	180
Db	121	SRGCAEQLTLGHLVHLKNDCHFELPCVRPDCKEKYLKRDLRHVEKACKYREATCSHC	180
QY	181	KSOYPMIALOKHEPDPCVYVSCPHKCSYQTLTIRSELTSAHLSGCVNAPSCSFRKVCY	240
Db	181	KSOYPMIALOKHEPDPCVYVSCPHKCSYQTLTIRSELTSAHLSGCVNAPSCSFRKVCY	240
QY	241	FOGTNOQIKAHASSAVOHVNLKEWNSLTKRYSLQNESVEKKNKSIOSLHNOICSPFI	300
Db	241	FOGTNOQIKAHASSAVOHVNLKEWNSLTKRYSLQNESVEKKNKSIOSLHNOICSPFI	300
QY	301	EIEROKEMLRNNEKSLIHLQVRIDSOAKELKELDKETRPFRQNMEEADSMKSYSVESIQNR	360
Db	301	EIEROKEMLRNNEKSLIHLQVRIDSOAKELKELDKETRPFRQNMEEADSMKSYSVESIQNR	360
QY	361	VTELESYDKSAGOVARNRTGLLESQLSRIDDQMLSVYHDIRLAMDRLFOYLEFASVNGVLIW	420
Db	361	VTELESYDKSAGOVARNRTGLLESQLSRIDDQMLSVYHDIRLAMDRLFOYLEFASVNGVLIW	420
QY	421	KIRIYKRRKQAVNGKTLISLYSQPFYTYGFETKMCARVYLNGDMGKSTHLSFVYIMRG	480
Db	421	KIRIYKRRKQAVNGKTLISLYSQPFYTYGFETKMCARVYLNGDMGKSTHLSFVYIMRG	480

DR Pfam: PF000097, zf-C3HC4, 1.  
DR Pfam: PF00917, MATH, 1.  
DR Pfam: PF02176, zf-TRAF, 2.  
DR SMART: SM00061, MATH, 1.

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DR SMART: SM00184; RING: 1.
DR PROSITE: PS00518; ZF_RING_1; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR PROSITE: PS50145; ZF_TRAF; 2.
DR ZINC-finger; Coiled coil; Repeat.
FT ZN_FING 67 76 RING-TYPE.
FT ZN_FING 134 189 TRAF-TYPE 1.
FT ZN_FING 190 248 TRAF-TYPE 2.
FT ZN_FING 266 337 COILED COIL (POTENTIAL).
FT DOMAIN 417 502 MATH/TRAF.
FT DOMAIN 72 73 CE -> MQ (IN REF. 2).
FT CONFLICT 390 390 T -> M (IN REF. 2).
FT CONFLICT 390 390 T -> M (IN REF. 2).
SO SEQUENCE 567 AA; 64263 MW; 2522B343B41192DC CRC64;

Query Match 96.0%; Score 2886.5; DB 1; Length 567;
Best Local Similarity 96.1%; Pred. No. 1,7e-165;
Matches 546; Conservative 7; Mismatches 14; Indels 1; Gaps 1;

OY 1 MESSKMDSPGALQNPPLKLTDRSAGTPVPEQGGYKKEFKYEDKCKCHLYL 60
DB 1 MESSKMDSPGALQNPPLKLTDRSAGTPVPEQGGYKKEFKYEDKCKCHLYL 59
OY 61 CSPKTEGCHRFECSCMAALLSSSSPKCTACQESIIVKDKVCKCKREILALQYCRNE 120
DB 60 CNPKTEGCHRFECSCMAALLSSSSPKCTACQESIIVKDKVCKCKREILALQYCRNE 119
OY 121 SRGCAEQLTLGHLVHLKNDCHFEELPCVPRDCKEYLRKLRDHYEAKCYRRAATCSHC 180
DB 120 GNGCAEQLTLGHLVHLKNDCHFEELPCVPRDCKEYLRKLRDHYEAKCYRRAATCSHC 179
OY 181 KSOVNMILQKHEDTDCPCVYVSCPHKCSVOTLLRSELSEHLSECVNAPSCSKRYGCV 240
DB 180 KSOVNMILQKHEDTDCPCVYVSCPHKCSVOTLLRSELSEHLSECVNAPSCSKRYGCV 239
OY 241 FOGTNOQIKAHBASAVOHVNLKEMSNLEKRVSLQNESVEKNKSIQSLHNOICSEFI 300
DB 240 FOGTNOQIKAHBASAVOHVNLKEMSNLEKRVSLQNESVEKNKSIQSLHNOICSEFI 299
OY 301 EIERKEMLRNNESKILHLQRYIDQAKELKEIRPFQNMEDASMSVSESLONR 360
DB 300 EIERKEMLRNNESKILHLQRYIDQAKELKEIRPFQNMEDASMSVSESLONR 359
OY 361 VTELSVDKSAQOVARNTGLSESLSRHDOMLVHDIRLADMDLRFQVLETASYNGVLIW 420
DB 360 VTELSVDKSAQOVARNTGLSESLSRHDOMLVHDIRLADMDLRFQVLETASYNGVLIW 419
OY 421 KIRDYKRRKQEAVMGKTLISLQPEYTYGFGYKMCARVYLANGDGKGTSLLEFVIMRG 480
DB 420 KIRDYKRRKQEAVMGKTLISLQPEYTYGFGYKMCARVYLANGDGKGTSLLEFVIMRG 479
OY 481 EYDALLPWFQKQVTLMLDQSSSRRLHGDARFPPNNSSPKPTGEMNINISGCPVFAVQ 540
DB 480 EYDALLPWFQKQVTLMLDQSSSRRLHGDARFPPNNSSPKPTGEMNINISGCPVFAVQ 539
OY 541 TVLENGTYIKDDTIFIKVIVTSDLPDP 568
DB 540 TVLENGTYIKDDTIFIKVIVTSDLPDP 567

RESULT 3
TRA2_MOUSE STANDARD: PRT: 501 AA.
ID TRA2_MOUSE
AC P39429;
DT 01-FEB-1995 (rel. 31, Created)
DT 01-FEB-1995 (rel. 31, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE TNF receptor associated factor 2 (TRAF2).
GN TRAF2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE-94349371; PubMed-8069916;
RA Rote M., Wong S.C., Henzel W.J., Goeddel D.V.;
RT "A novel family of putative signal transducers associated with the
RT cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";
RL Cell 78:681-692(1994).
CC -1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN
CC OF THE 75 KDA TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2) AND
CC ACTIVATES NF-KAPPA-B.
CC -1- SUBUNIT: HOMODIMER OR HETERODIMER OF TRAF1 AND TRAF2. THIS
CC HETERODIMER CAN BIND TO THE N-TERMINAL OF INHIBITOR OF APOPTOSIS
CC PROTEINS 1 AND 2 (IAPs), TO RECRUIT THEM TO THE TUMOR NECROSIS
CC FACTOR RECEPTOR 2 (TNFR2).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -1- SIMILARITY: CONTAINS 1 MATH/TRAF DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 TRAF-TYPE ZINC FINGERS.
CC -1- SIMILARITY: CONTAINS 2 TRAF-TYPE ZINC FINGERS.
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CC or send an email to license@isb-sdb.ch).
CC
CC EMBL: L35303; AAC37662.1; -
CC HSSP: P12351; 1HMT.
CC WGD: MG1101835; Traf2.
CC InterPro: IPR002083; MATH.
CC InterPro: IPR003007; TRAF.
CC InterPro: IPR001293; ZnF_TRAF.
CC InterPro: IPR001841; ZnF_fing.
CC Pfam: PF00097; ZF-C3HC4.1.
CC Pfam: PF00917; MATH; 1.
CC Pfam: PF02176; ZF-TRAF; 2.
CC SMART: SM00061; MATH; 1.
CC SMART: SM00184; RING; 1.
CC SMART: SM00518; ZF_RING_1; 1.
CC PROSITE: PS00518; ZF_RING_1; 1.
CC PROSITE: PS50089; ZF_RING_2; 1.
CC PROSITE: PS50145; ZF_TRAF; 2.
CC ZINC-finger; Coiled coil; Repeat.
CC ZN_FING 34 73 RING-TYPE.
CC ZN_FING 124 180 TRAF-TYPE 1.
CC ZN_FING 177 233 TRAF-TYPE 2.
CC DOMAIN 298 348 COILED COIL (POTENTIAL).
CC DOMAIN 334 501 MATH/TRAF.
CC SEQUENCE 501 AA; 56026 MW; 043B391180365F10 CRC64;

Query Match 27.8%; Score 837.5; DB 1; Length 501;
Best Local Similarity 33.6%; Pred. No. 3.5e-43;
Matches 196; Conservative 89; Mismatches 194; Indels 105; Gaps 17;

OY 3 SSKRMDSPGALQNPPLKLTDRSAGTPVPEQGGYKKEFKYEDKCKCHLYL 61
DB 2 AAASVTSFGSLLELP-----GSKTLGTRLEAKGLCAACKILR 42
OY 62 SPKTEGCHRFECSCMAALLSSSSPKCTAC-----QESI---VKQVFFDNCKKREILA 112
DB 43 RPFQAGCHRYCSFCLISLSSGPNCAACYBEGISLESSAFDNNARREVES 102
OY 113 LQIYCRNRCGAEQLTLGHLVHLKNDCHFEELPCVPRDCKEYLRKLRDHYEAKCY 172
DB 103 LPAYCPND--GCTWKGTLKEYESCHEGLCPILLTEC--PACKGLVRLSEKHNHTEDGCPK 158
OY 173 REATCSHCKSOVPMIALQKHEDTDCPCVYVSCPHKCSVOTLLRSELSEHLSECVNAPSC 232
DB 159 RSLSCORCAPCSHVDEIVHEV--CPKPEPLTG--DGCKKKIIPREFQDHYRACSKCYLC 216
OY 233 SFKRYGCVFOGTNOQIKAHBASAVOHVNLKEMSNLEKRVSLQNESVEKNKSIQSLHNOESV 282
DB 217 RFTVYGCSENVETENLDQHLREHLALL--LSSTLEQASRGTINQVGPPELLNQCOI 274

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QY 283 EKNKSIQSLHNOICSEFIEIEROKEMLRNNSKILHLQHVIDSQAELKELDKREIRPERQ 342  
 Db 275 LEQR-LATEFNIVCVLNREVER-----VAVTAECASQRRLDD----- 312  
 QY 343 NMEELASMSVSSELONRTELESVDKSGOVARNTGLLESQLSRHDQMLSVHDIRLADM 402  
 Db 313 -----KIEALSNNKVOOLE-----RSIGL-----KDLAMADL 338  
 QY 403 DLRFQVLETASYNGVLIWKIRIDYKRRKQDAVMGKTILSYSOPEYTGFGYKMKCARVYLNG 462  
 Db 339 EKVSELEVSTYDGVITKISDFTRRKQAVAGRPAPFYSRYGKMKCLAVYLNG 398  
 QY 463 DGMKGTHTSLFFVIMRGEYDALLPPEFKQKTYLMLDMOGSSRRHLGDAFKDPNNSSEK 522  
 Db 399 DGGRGTHSLFFVYVKKGPDALLQWPFQKTYLMLDLH-NNRHVIYDAFRPDVTSSEK 457  
 QY 523 KPTGEMNIASGCPVFAQVLE-NGTYIKDTIFIKYIVDTSD 565  
 Db 458 RPYSDMNINISGCPLEPCVSKMEKKNSTYRDDAIFIKAVDITGL 501

## RESULT 4

TRAF2\_HUMAN STANDARD: PRT: 501 AA.

AC 012933: 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE TNF receptor associated factor 2 (TRAF2) (Tumor necrosis factor type 2 receptor associated protein 3).  
 GN TRAF2 OR TRAF3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9536958; PubMed=7639698;  
 RA Song H.Y., Donner D.B.;  
 RT "Association of a ring finger protein with the cytoplasmic domain of the human type-2 tumor necrosis factor receptor.";  
 RL Biochem. J. 309:825-829(1995).  
 RN [2]  
 RP SEQUENCE OF 201-501 FROM N.A.  
 RX MEDLINE=94349371; PubMed=8069916;  
 RA Roche M., Wong S.C., Henzel W.J., Goeddel D.V.;  
 RT "A novel family of putative signal transducers associated with the cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";  
 RL Cell 78:681-692(1994).  
 CC -1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN OF THE 75 KDA TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2) AND ACTIVATES NF-KAPPA-B.  
 CC -1- SUBUNIT: HOMODIMER OR HETERODIMER OF TRAF1 AND TRAF2. THIS HETERODIMER CAN BIND TO THE N-TERMINAL OF INHIBITOR OF APOPTOSIS PROTEINS 1 AND 2 (IAPs), TO RECRUIT THEM TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 CC -1- SIMILARITY: CONTAINS 1 MATH/TRAF DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 2 TRAF-TYPE ZINC FINGERS.  
 CC -----  
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 CC -----  
 DR EMBL: U12597; AAA87706.1; -  
 DR GenBank: HGNC:12032; TRAF2.  
 DR MIM: 601895; -  
 DR InterPro: IPR002083; MATH.

DR InterPro: IPR003007; TRAF.  
 DR InterPro: IPR001293; Znf-TRAF.  
 DR InterPro: IPR001841; Znf-TRAF.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR Pfam: PF00917; MATH; 1.  
 DR Pfam: PF02176; zf-TRAF; 2.  
 DR SMART: SM00061; MATH; 1.  
 DR SMART: SM00184; RING; 1.  
 DR PROSITE: PS00518; ZF\_RING\_1; 2.  
 DR PROSITE: PS50089; ZF\_RING\_2; 1.  
 DR PROSITE: PS50145; ZF-TRAF; 2.  
 KW Zinc-finger; Coiled coil; Repeat.  
 FT ZN\_FING 34 73  
 FT ZN\_FING 124 180  
 FT ZN\_FING 177 233  
 FT ZN\_FING 299 348  
 FT DOMAIN 334 501  
 FT COILED COIL (POTENTIAL).  
 FT MATH/TRAF.  
 FT CONFLICT 343 365  
 FT RPFQACGHRVCSFCLASLIRKL -> LEMEASTYDGVITW  
 FT KISDFAPKR (IN REF. 2).  
 SQ SEQUENCE 501 AA; 55794 MW; 8883651EB6E20743 CRC64;

## Query Match

Best Local Similarity 24.7%; Score 744; DB 1; Length 501;  
 Matches 187; Conservative 86; Mismatches 186; Indels 98; Gaps 21;

QY 36 QGGYKEKFKVT-VEDKYKCEKHLYLCSPKQTEGHRFCESCAALLSSSPKCTAC-QE 93  
 Db 16 QPGRSKTLTGKTLBAKLYLSCARVLRPPQAOQGHRYCSFCLASLSSGPOMCACVHE 75  
 QY 94 SIYADKV-----FNDNCKRETLALQIYCRNESGCAQDLTGLHLVHLANDCHFE 145  
 Db 76 GIVEEGISLIESSSAFEDNAARREVESELPVC--PSDGYTKWGLKEY-----ESCHEGR 128  
 QY 146 LPCVR---PDCKEYVLRKLDLHVEKACKYREATCSHCKSQVPMIALQKHEDTDCVVY 202  
 Db 129 CFLMLECPACKGLVLRGEEKRHLEHCPEKRSLSCHRCRAPCCGADVKAHNEY-CRKFPL 187  
 QY 203 SCPRKCSYQTLTRELSENAHLSQVNPSTCSFKRYGV--FQGTNDQIKAHESNAVQY 260  
 Db 188 TC-DGCGKRRKIPREKFPDHYVTCGCRVPCRFHAIQGLTEVEGEKQ--EHEVQWLRHL 244  
 QY 261 NLKEMWSNLEKK-----VSILQ--EYVKNKSIQSLHNOICSEFIEIEROKEM 309  
 Db 245 AML--LSSVLEAKPLLDQSHAGSELQRCESLEKTA--TFENIVCVLNREVER----- 295  
 QY 310 RNNESKILHLQRYVDSQAELKELDKREIRPQWNEBADSMSVSSELONRTELESVDK 369  
 Db 296 -----VAMTAECAS-----RQHRLLDQ-----KIEALSNNKVOOLE----- 325  
 QY 370 SAGOVARTGLLESQLSRHDQMLSVHDIRLADMRLPQVLETASYNGVLIWKIRIDYKRR 429  
 Db 326 -----RSIGL-----KDLAMADLEOKYRPPQAOQGHRYCSFCLASLIRKL 365  
 QY 430 QEAVAGTSLSYSOPEYTGFGYKMKCARVYLNGMGKGTHTSLFFVIMRGEYDALLPMP 489  
 Db 366 QEAVAGTSLSYSOPEYTGFGYKMKCARVYLNGMGKGTHTSLFFVIMRGEYDALLPMP 425  
 QY 490 FKQKVTMLMDQSSRRHLGDAFKDPNNSSEKPTGEMNIASGCPVFAQVLE-NGTY 548  
 Db 426 FNQKVTMLMDQ--NNRHVIYDAFRPDVTSSEKFPVNDMNINISGCPLEPCVSKMEKKNST 484  
 QY 549 IKDITFIKIVDTSD 565  
 Db 485 VRDPAIFIKAVDITGL 501

## RESULT 5

TRAF2\_HUMAN STANDARD: PRT: 416 AA.  
 AC Q13077;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE TNF receptor associated factor 1 (TRAF1) (Epstein-Barr virus-induced protein 6).

DE TRAF1 OR EB16.

OS Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

CC NCBI\_TaxID=9606;

OX NCBI\_TaxID=9606;

RN (1)

RP SEQUENCE FROM N.A.

RC TISSUE=Lymphoma;

RX MEDLINE=95163092; PubMed=7859281;

RA Mosialos G., Birkenbach M., Yalamanchili R., Vanarsdale T., Ware C., Kleif E.;

RA "The Epstein-Barr virus transforming protein LMP1 engages signaling proteins for the tumor necrosis factor receptor family.";

RT Cell 80:389-399(1995).

CC -1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN OF THE 75 KDA TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2).

CC -1- SUBUNIT: HOMODIMER OR HETERODIMER OF TRAF1 AND TRAF2. THIS HETEROCOMPLEX CAN BIND TO THE N-TERMINAL OF INHIBITOR OF APOPTOSIS PROTEINS 1 AND 2 (IAPs), TO RECRUIT THEM TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- SIMILARITY: CONTAINS 1 MATH/TRAF DOMAIN.

CC -----

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CC -----

CC EMBL: U19261; AAA62309.1; -

CC DR Genev; HGNC:12031; TRAF1.

CC DR MIM: 601711; -

CC DR InterPro: IPR002083; MATH.

CC DR InterPro: IPR003007; TRAF.

CC DR Pfam: PF00917; MATH; 1.

CC DR SMART: SM00061; MATH; 1.

CC KW Coiled coil.

CC FT DOMAIN 182 264 COILED COIL (POTENTIAL).

CC FT DOMAIN 269 354 MATH/TRAF.

CC FT SEQUENCE 416 AA; 46163 MW; A956A123A40D284A CRC64;

CC SQ

Query Match 21.2%; Score 636.5; DB 1; Length 416;

Best Local Similarity 35.3%; Pred. No. 2,9e-31;

Matches 164; Conservative 72; Mismatches 126; Indels 103; Gaps 17;

DB 138 KNOCHHEILPCVPRDCKEYLRKDRDHYEACKYREATCSHCKSQVPMIALQKHEDTDC 197

DB 15 ENEPFGCGPTVCGDREKPE-----FALCAGAGLSNP-----RNGEDQIC'54

QY 198 PCVVVSCPHKCSVOTL-----LNSLSAHLSECVNAPSTCSFKRGCVFGGTNOQIK 249

DB 55 P-----KCRGEDIQISPGSRRLFTQEKAH-PEVAEAGICGPFAGVGSQSQSQVQ 105

QY 250 AHEASSAVOVNLL-----KEMS-----NSLEKVSILQ-NESEVKNKSIO-SLH 292

DB 106 EHEVTSQTHNLGLGFMKQMKARLGGLESGPMALFQNLSDQLQAAVYADDEVDQC 165

QY 293 NQICSEIEIEROKEMLRNNEKSKILHQRVIDSOAEKLEKLEIRPFRONMEADSMKS 352

DB 166 RAPSS-----ESQEE-----LALQHPM--KEKLLALEGLRIVF-----E 198

QY 353 SVESLQNRVTELESVDKSAQVARNITLLESQLSRH-----DQMLSVHDIRLA 400

DB 199 NIVAVLNKEVE-----ASHLATSIHOSQIDREIRILSEORVVELQDTLQKQDALG 251

QY 401 DMDLRFOVLETSYNGVLIWKIRDKRRKROEAVNGKTLISYQPFYTGEGYKMCARVYL 460

DB 252 KLEOSLRIMEASFDGFIWKITVTRRCHESACGRIVSLSPAFYTAQKGYKLCALTYL 311

QY 461 NGDGMKGTHTLSLFYIMNGEYDALLPMPKOKVTLMIMDQSSRRHLGDAFKPPDNNSS 520

DB 312 NGDGTCKRTHLSLFYIMNGEYDALLPMPKRNKVFEMILDQ--NNREHAIADARPLSSAS 370

QY 521 FKRPSEMIINASCPEVFAQVLEN--GTIYIDDTIFIRVIYDTS 563

DB 371 FQRPOSETVNASCPLFPLSKLQSPKHAHYVVDIMFLKICIVETS 415

RESULT 6

TRAF1\_MOUSE STANDARD; PRT; 409 AA.

AC P39428;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE TNF receptor associated factor 1 (TRAF1).

GN TRAF1.

OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

CC NCBI\_TaxID=10090;

CC [1]

CC SEQUENCE FROM N.A., AND SEQUENCE OF 123-135 AND 390-402.

CC MDLINE=94349371; PubMed=8065916;

CC RA Rothe M., Wong S.C., Henzel W.J., Goeddel D.V.;

CC "A novel family of putative signal transducers associated with the cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";

CC RT Cell 78:681-692(1994).

CC -1- FUNCTION: SIGNAL TRANSDUCER ASSOCIATED WITH THE CYTOPLASMIC DOMAIN OF THE 75 KDA TUMOR NECROSIS FACTOR RECEPTOR (TNF-R2). THIS HETEROCOMPLEX CAN BIND TO THE N-TERMINAL OF INHIBITOR OF APOPTOSIS PROTEINS 1 AND 2 (IAPs), TO RECRUIT THEM TO THE TUMOR NECROSIS FACTOR RECEPTOR 2 (TNFR2).

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- SIMILARITY: CONTAINS 1 MATH/TRAF DOMAIN.

CC -----

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CC -----

CC EMBL: L35302; AAC37663.1; -

CC DR MGD: MGI:101836; Traf1.

CC DR InterPro: IPR002083; MATH.

CC DR InterPro: IPR003007; TRAF.

CC DR Pfam: PF00917; MATH; 1.

CC DR SMART: SM00061; MATH; 1.

CC KW Coiled coil.

CC FT DOMAIN 167 256 COILED COIL (POTENTIAL).

CC FT DOMAIN 262 347 MATH/TRAF.

CC FT SEQUENCE 409 AA; 45464 MW; EBA7FEE539FEDDF CRC64;

CC SQ

Query Match 20.9%; Score 628; DB 1; Length 409;

Best Local Similarity 36.6%; Pred. No. 9e-31;

Matches 154; Conservative 69; Mismatches 128; Indels 70; Gaps 13;

DB 173 REATCSHCKSQVPMIALQKHEDTDCPCVVVSCPHKCSVOTLRLSELNHLSECVNAPSTC 232

DB 28 RVLCTACLSF-----NLKRDIEDRICKCADNHLHYSPSPITGP-KVN-SQVAAELMC 81

QY 233 SFKRGCVFGGTNOQIKAEASSAVOVNLL-----LKEMSNS-----LEKVSIL 277

DB 82 PFAGVGSFSGSPQSQMQHEATQSOSHLVLLAVLKEWSSPGSNGSPALLENLSEL 141

QY 278 QNESEVKNKSISQSLNQCISFEIEIEROKEMLRNNEKSKILHQRVIDSOAEK-LKEIDME 336

DB 142 Q-----LQAAVATGDELDVDCYRACCSQEBELALQHLVK-----EKLLOLEBK 186

QY 337 IRPFROMWEADSMKSSVESLQNRVTELSVDKAGOVARNITGLSELSRH----- 388  
 DB 187 LRVF-----ANIVAVLNKVE-----ASHLLALASINHSQDLRELLSLEOR 228  
 QY 389 -----DQMLSVHDIRLADMOLRFVOLTASTNGVLLWKINDYKRRKQEAVMGKTLISYOP 444  
 DB 229 VVELQOTLQOKDVLGKLEHSLRLMEASFDGTFMKITNVKRCHEVSCGRVSLFSPA 288  
 QY 445 FYTGYGFKKCAVYLNQDGMKGTLSTLFVIMRGEVALLPMPKOKVTMLMDQSS 504  
 DB 289 FYTAKGYVLCRLVYLNQDGMKGTLSTLFVIMRGEVALLPMPKOKVTMLMDQSS 347  
 QY 505 RRLHGAEPDPNSSFKKPTGEMINIASGCPVFAQVLEN--GTYIKDDTIFIRIYDT 562  
 DB 348 RHAIDAFRDLSSASFQRPQSETNVAAGCPLEFPLSKLQSPKHAIVDDTFLKCIYDT 407  
 QY 563 S 563  
 DB 408 S 408

## RESULT 7

DB17\_DICDI STANDARD: PRT: 458 AA.  
 AC P11467: 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE DG17 protein.  
 GN ZFAA OR DG17.  
 OS Dictyostelium discoideum (Slime mold).  
 OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.  
 NC NCB1\_TaxID=44689;  
 RN [1]  
 RX MEDLINE=88142840; PubMed=2830496;  
 RA DISCOLL D M, Williams J.G.;  
 RT "Two divergently transcribed genes of Dictyostelium discoideum are  
 RL cyclic AMP-inducible and coregulated during development.";  
 RL Mol. Cell. Biol. 7:4482-4489(1987).  
 CC -1- INDUCTION: BY CAMP DURING AGGREGATION.  
 CC -1- MISCELLANEOUS: THE EXPRESSION OF DG17 PROTEIN IS DEVELOPMENTALLY  
 CC REGULATED.  
 CC -1- SIMILARITY: CONTAINS 1 TRAF-TYPE ZINC FINGER.  
 CC  
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 CC  
 CC EMBL; M18106; AAA3192.1; -  
 DR PIR; A29361; A29361.  
 DR DictyDb; DD02010; zfaa.  
 DR InterPro; IPR002083; MAT.  
 DR InterPro; IPR001293; Zn1\_TRAF.  
 DR InterPro; IPR001841; Zn1\_fing.  
 DR Pfam; PF00917; MAT; 1.  
 DR Pfam; PF02176; zf-TRAF; 2.  
 DR SMART; SM00061; MAT; 1.  
 DR SMART; SM00184; KIN; 1.  
 DR SMART; PS0145; zf-TRAF; 1.  
 DR PROSITE; PS0145; zf-TRAF; 1.  
 KW Developmental protein; zinc-finger.  
 FT SIMILAR 25 67 TO DROSOPHILA SINA (AA 71-108).  
 FT ZN\_FING 27 66 POTENTIAL.  
 FT ZN\_FING 193 250 TRAF-type.  
 SO SEQUENCE 458 AA; 53015 MW; FE4804D9AB90EB26 CRC64;

Query Match 6.7%; Score 201; DB 1; Length 458;  
 Best Local Similarity 20.1%; Pred. No. 3;e-05;  
 Matches 115; Conservative 77; Mismatches 174; Indels 206; Gaps 28;

QY 48 EDKYCKECHLVLSPKQTEC--GHRFCESMAALLSSSPKCYACO-----ESI 95  
 DB 22 KNYKTCPICFEYIKKQIYQCKSGHHACKCEKESLFTKK-ECMTCKSVNYSNDLSRL 80  
 QY 96 VKDVF--KDMCC--KRELLAQIYC-----RNSRGAEDLTGHL 134  
 DB 81 MVERAFDEKKECCCIYSFNEQIVEGTCSPDGSAYONRNLIDENNGCKEKIEVDID 140  
 QY 135 VHLKNDCHFEELPCVRPDKREVLKRLRDHVEKACYREATCSHK--SOVPMIALQKH 193  
 DB 141 SHLIN-CQKRVYTSFNGC-EKILR--MNSIKNGEFKLVTDPCFRDRIKKLELTHY 195  
 QY 194 DTDCPCVAVSCPHGCSVOTLIRSELSAHLECVNAPSTCSFKRYGVOGTNOOIRAHNA 253  
 DB 196 KT-CPVAVIDCSQGSVKIERKSIIDHIDCCNTQIPCKYFEGC-----240  
 QY 254 SSAOVHNLKEMNSLEKRVSLQNESVEKNSISGLHQISFLEIRQKEMLRNNE 313  
 DB 241 -----KVMKRSLEQN-----251  
 QY 314 SKILHQRVIDSQAEKLEKDEIRPFROMWEADSMKSSVESLQNRVTELSVDKAG 373  
 DB 252 -----HLERV-----NHQNY-----MGLIERKLTQV-----GQ 275  
 QY 374 VARTGLLESQLSRHDM-----LSYHDIRLADMOLRFVOLTET--SYNGVL-TMKIR 423  
 DB 276 SKRT-----HDELLKRIEDLSLVYKFDACLKQVLEKALDICSNGYRNKWTIS 325  
 QY 424 DY-----KRRKQEAVMGKTLSTLYSOPFYTGFFYKMCARVYLNQDGMKGTLSTLFV 477  
 DB 326 NYSVAKSKINQALSPMLISLHLP-----QVC--VYRQGD--ENKEYSILYLRN 374  
 QY 478 -----MRGEYDALLPMPKOKVTMLMDQSSRRHLGDAKFPDPNSSFKKPTGEMNI 530  
 DB 375 NIEEPNSLAKVEYSFTL-----VNVLDKSKSIIRKED-----KKRVFISE 414  
 QY 531 ASGCPVFAQVTL--ENGYIKDDTIFIRIYIV 560  
 DB 415 GWGWRFLSLDLINKENGLSNDKLILBIYI 446

## RESULT 8

ID 2147 MOUSE STANDARD: PRT: 634 AA.  
 AC 061510: 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE zinc finger protein 147 (Tripartite motif protein 25) (Estrogen  
 DE responsive finger protein) (Efp).  
 GN ZNF147 OR TRIM25 OR ZFP147 OR EFP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NC NCB1\_TaxID=10090;  
 RN [1]  
 RX MEDLINE=96025835; PubMed=7592654;  
 RA Orlino A., Inoue S., Ikeda K., Noji S., Muramatsu M.;  
 RT "Molecular cloning, structure, and expression of mouse estrogen-  
 RT responsive finger protein Efp. Co-localization with estrogen receptor  
 RT mRNA in target organs.";  
 RL J. Biol. Chem. 270:24406-24413(1995).  
 CC -1- FUNCTION: MEDIATES ESTROGEN ACTION IN VARIOUS TARGET ORGANS.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 CC  
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CC EMBL, D63902; BAA09941.1; -  
 DR MGD; MG1:102749; Trlms2.  
 DR InterPro: IPR001870; Gamma\_carboxylase.  
 DR InterPro: IPR003878; SPRY\_domain.  
 DR InterPro: IPR003877; SPRY\_receptor.  
 DR InterPro: IPR001841; znf.fing.  
 DR Pfam: PF000697; zf-C3HC4; 1.  
 DR Pfam: PF00622; SPRY; 1.  
 DR SMART: SM00184; RING; 1.  
 DR SMART: SM00449; SPRY; 1.  
 DR PROSITE: PS00518; ZF\_RING\_1; 1.  
 DR PROSITE: PS00589; ZF\_RING\_2; 1.  
 DR Zinc-finger; Coll. coll.  
 KW ZN\_FING 13 RING-TYPE.  
 FT ZN\_FING 13 COILED COIL (POTENTIAL).  
 FT DOMAIN 215 305 SPRY.  
 FT DOMAIN 514 631 SPRY.  
 SQ SEQUENCE 634 AA; 71772 MW; 6695C9DE2832E611 CRC64;

Query Match 5.3%; Score 159; DB 1; Length 634;

Best Local Similarity 18.7%; Pred. No. 0.015;  
 Matches 75; Conservative 69; Mismatches 130; Indels 128; Gaps 17;

OY 49 DKYKCEKHLVLCSPKQTECGHRCESMAALLSSSP--KCTACQEST-VKDKVFKN- 104  
 DB 9 EELSCVCLLEPKRPVTPCGHNECTSLDETWVVOGPPYPCPOCRKYVQVAPOLAKNTV 68  
 OY 105 -CCKRE-----ILALQIVRNSSRGCAEOLTGHLVHLN 139  
 DB 69 MCAVVEOFLQAOARTPVDDWTPRPFSSANAOVACDH---CLTEIAKTCVLCMAS 124  
 OY 140 DC-----HFEELPCVRPCKEKVLRKDLRHERAK---KYRATCSHCKSGVPMIAL 189  
 DB 123 FQGHNLPRHPS-----PAFQHPLOSPRIIDLRRKCTQHNLRBFECF----- 168  
 OY 190 QKHEDTDCQVAVSCPHK-CSVQTLRLSELNHLSECVNAPSTCSFKRYGCGVFOGTNOI 248  
 DB 169 ---EHGECICICLVHKKCSPTTL--SQASADL----- 197  
 OY 249 KAHKSSAVOHNLLKEMNSLEKRVSLDNEVEKNKSIOSLHNOICSEIEIEROKEM 308  
 DB 198 -----EYKLRNKLTIMHSHINGATKALEVRSKQOCVDSMKRMKMQ 239  
 OY 309 LRNNESKILHLQVTD---SQAELKELDKEL-----RPFQNMFEADSMKSVES 356  
 DB 240 LR---OEYEMKAVIDAETSSLRLRLEKEKRYGKFTDIYGVLVKKSEMOKLAEVEL 296  
 OY 357 LONRVTELESVSKSA---GOVARNTEGLLSQLSRHDQMLSVH 395  
 DB 297 IMDKGEFELEKAKLQESIKRYVYIPIKIDD-HOLINGIV 337

# RESULT 9

MEPB\_MOUSE STANDARD: PRT: 704 AA.

AC 061847;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Meprin A beta-subunit precursor (EC 3.4.24.18) (Endopeptidase-2).  
 GN MEBP OR MEP-1B.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Kidney.  
 RC MEDLINE=94012651; PubMed=8407940;  
 RA Gorbee C.M., Marchand P., Jiang W., Copeland N.G., Gilbert D.J.,

RA Jenkins N.A., Bond J.S.;  
 RT "Cloning, expression, and chromosomal localization of the mouse  
 RT meprin beta subunit.";  
 RL J. Biol. Chem. 268:21035-21043(1993).  
 RN (2)  
 RN SEQUENCE FROM N.A. (ISOFORM BETA').  
 RC TISSUE=Kidney;  
 RX MEDLINE=96147211; PubMed=8567689;  
 RA Dietrich J.M., Bond J.S., Jiang W.;  
 RT "A novel meprin beta' mRNA in mouse embryonal and human colon  
 RT carcinoma cells.";  
 RL J. Biol. Chem. 271:2271-2278(1996).  
 CC -1 CATALYTIC ACTIVITY: Hydrolysis of protein and peptide substrates  
 CC preferentially on carboxyl side of hydrophobic residues.  
 CC -1 COPOLYMER: BINDS 1 ZINC ION.  
 CC -1 SUBUNIT: HETEROTETRAMER OF TWO ALPHA AND TWO BETA SUBUNITS WHICH  
 CC IS FORMED BY THE NON-COVALENT ASSOCIATION OF TWO DISULFIDE-LINKED  
 CC HETERODIMERS.  
 CC -1 SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1 ALTERNATIVE PRODUCTS: 2 ISOFORMS, THE BETA AND BETA' SUBUNITS, AND  
 CC DIFFER IN THEIR N-TERMINUS DUE TO DIFFERENTIAL PROMOTER USAGE AND  
 CC ALTERNATIVE SPLICING.  
 CC -1 TISSUE SPECIFICITY: THE BETA-SUBUNIT IS EXPRESSED IN KIDNEY,  
 CC INTESTINAL BRUSH BORDERS, AND SALIVARY DUCTS. THE BETA'-ISOFORM  
 CC HAS BEEN FOUND IN CARCINOMA CELLS.  
 CC -1 INDUCTION: By retinoic acid.  
 CC -1 PTM: THIS PROTEIN UNDERGOES PROTEOLYTIC PROCESSING. BOTH FORMS  
 CC ARE GLYCOSYLATED.  
 CC -1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.  
 CC -1 SIMILARITY: CONTAINS 1 MAM DOMAIN.  
 CC -1 SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.  
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CC EMBL: L15193; AAA75234.1; -  
 DR HSP; P28825; IIAF.  
 DR MEROPS; M12.004; -.  
 DR MGD; MG1:96964; Mep1b.  
 DR InterPro: IPR001506; Astacin.  
 DR InterPro: IPR000561; EGF-like.  
 DR InterPro: IPR000998; MAM\_domain.  
 DR InterPro: IPR002083; MATH.  
 DR InterPro: IPR003007; TRAF.  
 DR InterPro: IPR000130; Zn\_MTPeptide.  
 DR Pfam: PF00008; EGF; 1.  
 DR Pfam: PF00629; MAM; 1.  
 DR Pfam: PF00917; MATH; 1.  
 DR Pfam: PF01400; Astacin; 1.  
 DR PRINTS: PR00480; ASTACIN.  
 DR PRINTS: PR00020; MAMDOMAIN.  
 DR SMART: SM00181; EGF; 1.  
 DR SMART: SM00137; MAM; 1.  
 DR SMART: SM00661; MATH; 1.  
 DR SMART: SM00235; znmc; 1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; 1.  
 DR PROSITE: PS00740; MAM\_1; 1.  
 DR PROSITE: PS00600; MAM\_2; 1.  
 DR PROSITE: PS00022; EGF\_1; FALSE\_NG.  
 DR PROSITE: PS01186; EGF\_2; FALSE\_NG.  
 KW Transmembrane; Hydrolase; Metalloprotease; Zinc; Glycoprotein;  
 KW Zymogen; Signal; EGF-like domain; Alternative splicing.  
 FT SIGNAL 1 20  
 FT PROPEP 21 64  
 FT CHAIN 65 704  
 FT DOMAIN 21 654  
 FT TRANSMEM 655 678  
 FT DOMAIN 679 704  
 BY SIMILARITY.  
 MEBPIN A BETA-SUBUNIT.  
 EXTRACELLULAR (POTENTIAL).  
 POTENTIAL.  
 CYTOPLASMIC (POTENTIAL).



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FT DOMAIN 63 260 METALLOPROTEASE.
FT DOMAIN 601 430 MAM.
FT DOMAIN 607 467 EGF-LIKE.
FT METAL 153 153 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT SITE 154 154 BY SIMILARITY.
FT METAL 157 157 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 163 163 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 611 622 BY SIMILARITY.
FT DISULFID 616 631 BY SIMILARITY.
FT DISULFID 633 646 BY SIMILARITY.
FT CARBOHYD 193 193 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 219 219 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 255 255 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 316 316 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 422 422 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 437 437 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 529 529 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 548 548 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 593 593 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT VARSPLIC 1 27 MDARQPMVEAFATFLASGLPAPEKE -> MNSTAGPASR
SRHSFKCRMKLLKAPRDGMVMTFG (IN ISOBOM
BETA').
SQ SEQUENCE 704 AA; 79548 MW; 2D610EDD74650F70 CRC64;

Query Match 5.0%; Score 151.5; DB 1; Length 704;
Best Local Similarity 25.1%; Pred. No. 0.049;
Matches 54; Conservative 38; Mismatches 56; Indels 67; Gaps 11;

OY 392 LSVHDIRLMDMLRFQVETASTYNGVLIMKIDYKRRQGEVMTGLSYSQPEFTGFG 451
DB 416 LSIIDINISSETCRPH-----IWHIONF-----TOLIGODITSVSPFYSSK-G 459
OY 452 YKMCARVYLINGDGKGGKTHLSFEVIMRGEYDALLPWPFR-QKXTLMDQ----- 501
DB 460 YAF-QIYMD--LRYSTNVGIYFHLISGANDDQLQMPQOQATMTLLDQNPDIRQME 514
OY 502 -----GS-----SRHIGDAFKPDNPSSSKRPPGEMNIAISGCPVPAQ 540
DB 515 NORSTTPMTSDNGSTFWMRPSKVGVTDF--PNTGFSR-----GIYGTVFTR 566
OY 541 TVLENGYIKDDTFIRKIVD-----TSDLPDP 568
DB 567 ERLKSRERIKGDYITLLTVEDISHLNSTSAVDP 601

RESULT 10
RA50_METUA STANDARD; PRT; 1005 AA.
ID RA50_METUA
AC Q58718;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA double-strand break repair rad50 ATPase.
GN RAD50 OR MJ1322.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcales; Methanocaldococcus.
ON NCBI_TaxID=2190;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RA MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kierlavage A.R., Dougherty B.A., Tomb J.F., Adams R.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Georgiades N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Bordovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii."
RL Science 273:1058-1073(1996).

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CC -1- FUNCTION: Involved in DNA double-strand break repair (DSBR). The
CC rad50/mre11 complex possesses single-strand endonuclease activity
CC and ATP-dependent double-strand-specific exonuclease activity.
CC Rad50 provides an ATP-dependent control of mre11 by unwinding
CC and/or repositioning DNA ends into the mre11 active site (By
CC similarity).
CC -1- SUBUNIT: Forms a complex with mre11 (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.
CC
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CC
CC EMBL: U67572; AAB99331.1; -.
CC TIGR: MJ1322; -.
CC DR InterPro: IPR003439; ABC_transport.
CC DR InterPro: IPR003405; SMC_C.
CC DR InterPro: IPR003395; SMC_N.
CC DR Pfam: PF02463; SMC_N; 1.
CC DR Pfam: PF02483; SMC_C; 1.
CC DR ProDom: PD000006; ABC_transport; 1.
CC KW DNA repair; Hydrolase; ATP-binding; Coiled coil; Complete proteome.
CC NP_BIND 32 39 ATP (By similarity).
CC FT DOMAIN 158 849 COILED COIL (POTENTIAL).
CC FT SEQUENCE 1005 AA; 119387 MW; 9BBB48173E78B53 CRC64;

Query Match 5.0%; Score 150; DB 1; Length 1005;
Best Local Similarity 19.8%; Pred. No. 0.09;
Matches 73; Conservative 77; Mismatches 102; Indels 116; Gaps 18;

OY 130 LGHLVHLKNDCHFEELPCVRPCKEYVLRKIDRHYEAKCKRYATGCHSGSVPMAAL 189
DB 346 LDTLLNKIKDE--IERETIK-DLLEEL--KNLNEIEIKETKYR-ICECKEY----- 393
OY 190 QKHEDTDCPCVVVSPHKCSVOTLNLSELSAHLSECVNAPSTCSFRCVCGTNOQIK 249
DB 394 -----YKTY-----LELEK 403
OY 250 AHEASS-AVOHNLKEMWSLSLEKYSVLQ--NESVE--KNKSIOSLHNOJSEFEIEE 303
DB 404 AVEYNKLTLEYITLQD--KKSIEKINIDLETRINKLLEFKNIDISINSL-----KEIE 458
OY 304 ROKEMLRNNSKTLIHQR--VIDSQAEKLEKDEIR-----PRQNMEEADS 349
DB 459 EKKRVLENLOKEKTELEKKEINSEIKRUKKTLDELKEVEGKCPCKTPIDEN--KKMEL 517
OY 350 MKSSVSLQNRVELESVDKSAQAVARNTGLLESQLSRHDQMLSYDIRLADMDLRFQVL 409
DB 518 INGHKTQNLNKKYELKEIKKRIREIKDEIKKELEKDEKRENKLT-----LKTLYL 567
OY 410 ETASTYNGVLIWKTRDYKRRKQEARVMGKTLISL--SQPF-----YTGYSFGK 453
DB 568 EKQSOIELEELKLNKYEKQDLE--INKKISNYVINGKPYDEILIEDIKSQLNKFKMYNOY 625
OY 454 MCARYLYN 461
DB 626 LSAVSYLN 633

RESULT 11
RA50_AERPE STANDARD; PRT; 919 AA.
ID RA50_AERPE
AC Q9YFZ1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA double-strand break repair rad50 ATPase.
GN RAD50 OR APE0110.
OS Aeropyrum pernix.

```



Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;  
 CC Desulfurococcales; Aeropyrum.  
 CC NCBI\_TaxID=56636;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K1;  
 CC MEDLINE=99310339; PubMed=10382966;  
 RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Halkawa Y.,  
 RA Jlin K., Takahashi M., Sekine M., Baba S.-I., Anka A., Kosugi H.,  
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,  
 RA Takamaya M., Maeda S., Funahashi T., Tanaka T., Kubota K.,  
 RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,  
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;  
 RT "Complete genome sequence of an aerobic hyper-thermophilic  
 RT crenarchaeon, Aeropyrum pernix K1.";  
 RL DNA Res. 6:83-101(1999).  
 CC -1- FUNCTION: Involved in DNA double-strand break repair (DSBR). The  
 CC rad50/mre11 complex possesses single-strand endonuclease activity  
 CC and ATP-dependent double-strand-specific exonuclease activity.  
 CC Rad50 provides an ATP-dependent control of mre11 by unwinding  
 CC and/or repositioning DNA ends into the mre11 active site (by  
 CC similarity).  
 CC -1- SUBUNIT: Forms a complex with mre11 (by similarity).  
 CC -1- SIMILARITY: BELONGS TO THE SMC FAMILY RAD50 SUBFAMILY.  
 CC  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC  
 CC EMBL: AP000058; BAA79020.1;  
 DR InterPro: IPR003439; ABC\_transportr.  
 DR InterPro: IPR003405; SMC\_C.  
 DR InterPro: IPR003395; SMC\_N.  
 DR Pfam: PF02463; SMC\_N; 1.  
 DR Pfam: PF02483; SMC\_C; 1.  
 DR DNA repair; Hydrolyase; ATP-binding; Coiled coil; Complete proteome.  
 NP\_BIND 31 38 ATP (by SIMILARITY).  
 FT DOMAIN 202 758 COILED COIL (POTENTIAL).  
 FT SEQUENCE 919 AA: 104138 MW: 784480EB601B9DD CRC64;  
 SQ  
 Query Match 5.0%; Score 149.5; DB 1; Length 919;  
 Best Local Similarity 21.1%; Pred. No. 0.087;  
 Matches 90; Conservative 63; Mismatches 157; Indels 117; Gaps 15;  
 QY 61 CSKRCGCHRCSCSMALLSSSPKCAQCESTYKDKVFCNDCKREILALQYCR-- 118  
 DB 402 CSHKDL-CGSEKPEVLERL-----DAVINLESARALDQASLLEAARRL 448  
 QY 119 -----NSRGCAGQLTGLHLVHLKNDCHFEELPCVPDCKEYLRKLDHVEKACK 171  
 DB 449 VQALSMLESGSGARCPVG-----AELPPGAAEIAIRYRHE-AERLRKAAK 495  
 QY 172 YREATCSHCKSOVPMIALOKHEPTDPCVYVSCPRKCSQTLIR--SELSAHLSECYNAP 229  
 DB 496 EKAAEEKARAEASRLQDQRRR-----TELLSRLNQLEGLR----- 534  
 QY 230 STCSFRYCGVFGCTNQQAHAHASSAV--OHVVLKEMSNSELEKRVSLQNSYV---EK 284  
 DB 535 -----LGFOTPEDLAKAEOKLMLBERLEKLKLENSLEKRVNLSREVALREAK 585  
 QY 285 NKSISLHNOICSFETIEROKMLNNNSKILHLQRTVDSQAEKL----- 330  
 DB 586 TRALEVLQR---LGIKKEPARREKTLTSESKRLERMLVSKMEDLATRLGITAYRSLD 641  
 QY 331 -----KEL---DKETPRPROMNEEDSKSSVESIQNVTELESYDAGV 374  
 DB 642 LLEKARALEGVDELKSAIERLEARRLEAKLRKEAOKLKEWQYMKLELEAEKLRKE 701  
 QY 375 ARMTGLLESQLSRHDQMLSVHDIRLADMRLRFVLETAASYNGVLKIRDKRRKOEAAY 434

DB 702 VSRKSEIERKLEQVONTLAEEDDRISRIDRENGELQ-----RRREMSRK--ASG 750  
 QY 435 GKTLSDLY 441  
 DB 751 EEALRLY 757  
 RESULT 12  
 LMA4\_MOUSE  
 ID LMA4\_MOUSE STANDARD: PRT: 1816 AA.  
 AC P97927; P70409; O88785;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Laminin alpha-4 chain precursor.  
 GN LAMA4.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 462-469; 478-483; 776-782 AND  
 RP 940-945.  
 RC STRAIN=BALB/C; TISSUE=Endothelial cells;  
 RX MEDLINE=97363207; PubMed=9219532;  
 RA Frieser M., Noeckel H., Pausch F., Roeder C., Hahn A., Deutzmann R.,  
 RA Sorokin L.M.;  
 RT "Cloning of the mouse laminin alpha 4 cDNA. Expression in a subset of  
 RT endothelium.";  
 RL Eur. J. Biochem. 246:727-735(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Heart;  
 RX MEDLINE=97202462; PubMed=9049981;  
 RA Liu J., Mayne R.;  
 RT "The complete cDNA coding sequence and tissue-specific expression of  
 RT the mouse laminin alpha 4 chain.";  
 RL Matrix Biol. 15:433-437(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C;  
 RX MEDLINE=98010627; PubMed=9346933;  
 RA Iivanainen A., Korteseaa J., Sahlborg C., Morita T., Bergmann U.,  
 RA Thesleff I., Tryggvason K.;  
 RT "Primary structure, developmental expression, and immunolocalization  
 RT of the murine laminin alpha4 chain.";  
 RL J. Biol. Chem. 272:27862-27868(1997).  
 RN [4]  
 RP SEQUENCE OF 836-1106 FROM N.A.  
 RC STRAIN=ICR; TISSUE=Placenta;  
 RX MEDLINE=97296337; PubMed=9151674;  
 RA Miner J.H., Patton B.L., Lentz S.I., Gilbert D.J., Snider W.D.,  
 RA Jenkins N.A., Copeland N.G., Sanes J.R.;  
 RT "The laminin alpha chains: expression, developmental transitions, and  
 RT chromosomal locations of alpha1-5, identification of heterotrimeric  
 RT laminins 8-11, and cloning of a novel alpha3 isoform.";  
 RL J. Cell Biol. 137:685-702(1997).  
 RN [5]  
 RP SEQUENCE OF 1467-1691 FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=97187457; PubMed=9034910;  
 RA Lentz S.I., Miner J.H., Sanes J.R., Snider W.D.;  
 RT "Distribution of the ten known laminin chains in the pathways and  
 RT targets of developing sensory axons.";  
 RL J. Comp. Neurol. 378:547-561(1997).  
 CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin  
 CC is thought to mediate the attachment, migration, and organization  
 CC of cells into tissues during embryonic development by interacting  
 CC with other extracellular matrix components.  
 CC -1- SUBUNIT: Laminin is a complex glycoprotein, consisting of three  
 CC different polypeptide chains (alpha, beta, gamma), which are bound  
 CC to each other by disulfide bonds into a cross-shaped molecule

CC	CC	Completing one long and three short arms with globules at each end.
CC	CC	-1- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT MEMBRANES (MAJOR COMPONENT).
CC	CC	-1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN PERIPHERAL NERVES, CARDIAC MUSCLE, FAT, DERMIS, LUNG STROMA, AORTIC ENDOTHELIUM, ENDOCARDIUM AND ENDOTHELIUM OF BLOOD VESSELS IN SKIN AND BRAIN.
CC	CC	-1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
CC	CC	-1- DOMAIN: DOMAIN G IS GLOBULAR.
CC	CC	-1- SIMILARITY: CONTAINS 3.5 LAMININ EGF-LIKE DOMAINS.
CC	CC	-1- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
CC	CC	-----
CC	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/or_send_an_email_to_licenselsib-sib.ch">http://www.isb-sib.ch/announce/or_send_an_email_to_licenselsib-sib.ch</a> ).
CC	CC	-----
DR	DR	EMBL; U59850; ABA1840.1; -
DR	DR	EMBL; Y09827; CAA70970.1; -
DR	DR	EMBL; U59865; AAC324725.1; -
DR	DR	EMBL; U88352; AAC33178.1; -
DR	DR	EMBL; U69176; AAC32962.1; -
DR	DR	HSSP; P02468; IKLO.
DR	DR	MGD; MGI:109321; Lama4.
DR	DR	InterPro; IPR000561; EGF-like.
DR	DR	InterPro; IPR002049; Laminln_EGF.
DR	DR	InterPro; IPR001791; Laminln_G.
DR	DR	Pfam; PF00054; laminln_EGF; 3.
DR	DR	Pfam; PF00054; laminln_G; 4.
DR	DR	SMART; SM00181; EGF; 3.
DR	DR	PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR	DR	PROSITE; PS01248; LAMININ_TYPE_EGF; 3.
DR	DR	PROSITE; PS50025; LAM_G_DOMAIN; 5.
KW	KW	Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW	KW	Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT	FT	SIGNAL 1 24 POTENTIAL.
FT	FT	CHAIN 25 1816 LAMININ ALPHA-4 CHAIN.
FT	FT	DOMAIN 82 131 LAMININ EGF-LIKE 1.
FT	FT	DOMAIN 132 186 LAMININ EGF-LIKE 2.
FT	FT	DOMAIN 187 240 LAMININ EGF-LIKE 3.
FT	FT	DOMAIN 241 255 LAMININ EGF-LIKE 4 (INCOMPLETE).
FT	FT	DOMAIN 256 825 DOMAIN II AND I.
FT	FT	DOMAIN 826 1030 LAMININ G-LIKE 1.
FT	FT	DOMAIN 1042 1222 LAMININ G-LIKE 2.
FT	FT	DOMAIN 1229 1397 LAMININ G-LIKE 3.
FT	FT	DOMAIN 1462 1633 LAMININ G-LIKE 4.
FT	FT	DOMAIN 1640 1813 LAMININ G-LIKE 5.
FT	FT	DOMAIN 431 523 COILED COIL (POTENTIAL).
FT	FT	DOMAIN 556 604 COILED COIL (POTENTIAL).
FT	FT	DOMAIN 655 717 COILED COIL (POTENTIAL).
FT	FT	DOMAIN 770 799 COILED COIL (POTENTIAL).
FT	FT	DOMAIN 717 719 CELL ATTACHMENT SITE (POTENTIAL).
FT	FT	SITE 717 719 BY SIMILARITY.
FT	FT	DISULFID 82 91 BY SIMILARITY.
FT	FT	DISULFID 84 98 BY SIMILARITY.
FT	FT	DISULFID 101 110 BY SIMILARITY.
FT	FT	DISULFID 113 129 BY SIMILARITY.
FT	FT	DISULFID 132 146 BY SIMILARITY.
FT	FT	DISULFID 134 155 BY SIMILARITY.
FT	FT	DISULFID 157 166 BY SIMILARITY.
FT	FT	DISULFID 169 184 BY SIMILARITY.
FT	FT	DISULFID 187 202 BY SIMILARITY.
FT	FT	DISULFID 189 209 BY SIMILARITY.
FT	FT	DISULFID 212 221 BY SIMILARITY.
FT	FT	DISULFID 224 238 BY SIMILARITY.
FT	FT	DISULFID 266 266 INTERCHAIN (PROBABLE).
FT	FT	DISULFID 269 269 INTERCHAIN (PROBABLE).
FT	FT	CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	FT	CARBOHYD 308 308 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT	CARBOHYD	333	333	N-LINKED	(GLCNAC .)	(POTENTIAL)
FT	CARBOHYD	458	458	N-LINKED	(GLCNAC .)	(POTENTIAL)
FT	CARBOHYD	550	550	N-LINKED	(GLCNAC .)	(POTENTIAL)
FT	CARBOHYD	571	571	N-LINKED	(GLCNAC .)	(POTENTIAL)
FT	CARBOHYD	574	574	N-LINKED	(GLCNAC .)	(POTENTIAL)
FT	CARBOHYD	631	631	N-LINKED	(GLCNAC .)	(POTENTIAL)
FT	CARBOHYD	639	639	N-LINKED	(GLCNAC .)	(POTENTIAL)
FT	CARBOHYD	735	735	N-LINKED	(GLCNAC .)	(POTENTIAL)
FT	CARBOHYD	751	751	N-LINKED	(GLCNAC .)	(POTENTIAL)
FT	CARBOHYD	754	754	N-LINKED	(GLCNAC .)	(POTENTIAL)
FT	CARBOHYD	803	803	N-LINKED	(GLCNAC .)	(POTENTIAL)
FT	CARBOHYD	1088	1088	N-LINKED	(GLCNAC .)	(POTENTIAL)
FT	CARBOHYD	1283	1283	N-LINKED	(GLCNAC .)	(POTENTIAL)
FT	CARBOHYD	1361	1361	N-LINKED	(GLCNAC .)	(POTENTIAL)
FT	CONFLICT	8	8	C -> S (IN REF. 2)		
FT	CONFLICT	18	18	C -> Y (IN REF. 2)		
FT	CONFLICT	248	248	C -> R (IN REF. 3)		
FT	CONFLICT	297	297	G -> A (IN REF. 3)		
FT	CONFLICT	431	433	THR -> HPS (IN REF. 2)		
FT	CONFLICT	679	679	S -> C (IN REF. 3)		
FT	CONFLICT	703	703	D -> G (IN REF. 2)		
FT	CONFLICT	706	706	N -> H (IN REF. 2)		
FT	CONFLICT	728	728	K -> R (IN REF. 2)		
FT	CONFLICT	730	730	R -> I (IN REF. 2)		
FT	CONFLICT	779	779	F -> G (IN REF. 1)	AA SEQUENCE	
FT	CONFLICT	810	810	R -> S (IN REF. 3)		
FT	CONFLICT	865	867	ABP -> OT (IN REF. 2)		
FT	CONFLICT	936	936	K -> E (IN REF. 3)		
FT	CONFLICT	970	970	L -> V (IN REF. 3)		
FT	CONFLICT	1132	1132	H -> R (IN REF. 2)		
FT	CONFLICT	1200	1200	F -> I (IN REF. 2)		
FT	CONFLICT	1382	1382	D -> A (IN REF. 2)		
FT	CONFLICT	1413	1414	NS -> EF (IN REF. 1)		
FT	CONFLICT	1489	1489	A -> S (IN REF. 2)		
SO	SEQUENCE	1816 AA;	201818 MW;	B49C45F3A4599D8 CRC64;		
Query Match						
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Matches 104;		Conservative 75;	Mismatches 214;	Indels 137;	Gaps	24;
Oy	2	ESSKMDPSGALQTNPEPLKLTHTDRSAGTFVFPEDGGYKEKVKVYEDKKYKKECHLYLC	61			
Db	46	DSEISDSQVTTIGRLPPAERCDD--AG-----FFRTLSG--ECAPCD--C	84			
Oy	62	SPKQTEC--GARFPCSMALLSSSPKTAQESIVKDV-----FKDNC-----	105			
Db	85	NQNSHECIDLGSFCLHQCR--NTTGEHCEKLDIYIGDSINGTFRFOCPCPPLHLAN	141			
Oy	106	-----CKRETLAQIYICRNSRG-----CAEQLTLHLVH--LKNDCHFEELP--CVRPD	152			
Db	142	FAESCYFRKGAARCCICKENYVPGNCERCAPGYGNPMLLIGSTCKKCDSCGNSDPMIFED	201			
Oy	153	CKEYVLKRLDRVHAKCK--YREATCSHCKSQVPMIALQKHEDPDCVAVVSC--PHRCS	209			
Db	202	C-----DEITGQCRNCLANTTGGKCEKCAP--GYGDARTAKMCAYCNGGCPCD	249			
Oy	210	VQTLRLSELIAHLSECVNAPSTCSFKRYGCVPQGTNO-----QINAREHSS	255			
Db	250	-----SVTGECLIEGFEVPTGCD---KCVWDLTDRLALALSTEEKSGLLSVSSGAA	299			
Oy	256	AVOHNVNLKEMSNLSLEKRVSLLONSVAKNKSIGSLNHQOTSFELEF-----RQK	306			
Db	300	AHRHTVDMNSTIHLTRLTSLERENQYTLRKTIQINNSENTRLSLPVDVGLHEKGSQASRK	359			
Oy	307	EMLRNNE-----KLHLQRYIDSOAEKLTLEKDEIRFERNWE-----EADSM	350			
Db	360	GMIVAKESMDIITDATHLVEQAHNKKDIQIQLINSMKLYIGENQELGPETIAEKIYLAQMK	419			
Oy	351	KSSVESLQNRVTELESYDKSAGQVARNITGLSOLSRHD-----QMLSVYHDIRLA	400			
Db	420	LEETRSPQPLTLHRELVDEADEAQEILLQAEENMORLHNDTRSLFPPVYLQGLDDYINAKLS	479			

QY 401 DMDLRF-----QVLETSYNGVLIWKIRDYKR-----KQEAVMGKTLISL 440  
 DB 480 DQESINADLHVADNADNMRAITFRQDRHEKQHEKVEKQMEVVGASLGM 529  
 RESULT 13  
 ID YD86 SCHPO STANDARD; PRT; 1957 AA.  
 AC Q10411:  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hypothetical protein Clif3.06c in chromosome 1.  
 GN SPAC1F3.06c.  
 OS Schizosaccharomyces pombe (fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomyces.  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE=21848401; PubMed=11859360;  
 RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodson G.,  
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skellton J., Simmonds M., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Volkheart G., Aert R., Robben J., Grymopre B.,  
 RA Maltrens I., Vanstreets E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Puchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Medler H., Gloux S., Leleure V., Mottler S.,  
 RA Goffeau A., Cadieu E., Dreano S., Hunt C., Moore K., Hurst S.M.,  
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
 RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;  
 RA "The genome sequence of Schizosaccharomyces pombe."  
 RL Nature 415:871-880(2002).  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC  
 DR EMBL: 270690; CAA94624.1;  
 KW Hypothetical protein.  
 SQ SEQUENCE 1957 AA; 22785 MW; 3FA80CA06171D9DA CRC64;  
 Query Match 4.9%; Score 148; DB 1; Length 1957;  
 Best Local Similarity 20.3%; Pred. No. 0.26; Indels 174; Gaps 23;  
 Matches 105; Conservative 83; Mismatches 156;  
 QY 40 KEKFKVTEDEKYKCECHVILCSKQTECGHRCESCAALLSSSPCTACQESI-----95  
 DB 1416 KESLISLERS-----LSNQROKESLIDAKNELHMDPISRKNSLMEKTESIN 1466  
 QY 96 --VKDKVKNCKCKRETLAQICRNESRGCAEQ-----TLGHL 134  
 DB 1467 SLLDKSFELASVKEKIGALQ-KLHSESLSLMEINISQLOEAKKIQVDESTIOELDHEI 1525

QY 135 VHLKNDHFELPCVRDCKEYLRKDLRDHYKACKYREATCSHCKSOVPMIALOKHED 194  
 DB 1526 TASKN- NYEG-----KLNDKDSIIR-DLSNIEQL-----NNLIAEKSAYKRLSTEKSE 1574  
 QY 195 -----TDCPCVYVSCPHKCSQVOTLL-RSELSAHLSECVNAPSTCSFKRYGCVFGCTN 245  
 DB 1575 ILQENSRLADLEY-----HKSOVESLGRSKLK-----LASTT 1607  
 QY 246 OIKRAHE-----ASSAVOHVNLLEKWSN-----SLEKKYSLLONESYEKKK 286  
 DB 1608 EELQIAENERSLITPTRMDDLONOVKYKDLSDLSKEDLRLKSLSESVASLQKECKIKSN 1667  
 QY 287 SIQSLANDICS-----FELIEIRQKEMIRNNSEKILIHQVYDSQAEKLKELDKETRP 339  
 DB 1668 TVESLQDVLTVQARNAELEDESVSRVDKIRRDREHL-----SGKLKILHSQLEE 1720  
 QY 340 FRQNMEDADSMKSSVESLQNNRYTELESYKDSAGOVARNITGLSESQSLRHQOMLSYHDRL 359  
 DB 1721 QHETFFRAE-----QQRMTQL-----GFLKETVYKQEKRLKLNLRQ 1757  
 QY 400 ADMDLRFQVLETSYNGVLIWKIRDYKR-----KQEAVMGKTLISLSDPEYGYGYKKA 456  
 DB 1758 EQLIPRSSILYVESY-----IRDIKEIILYLOERLNGIEL-----SQQLPKGYFGY-----1803  
 QY 457 RYVLNDDGKMGKTHLSLFFVIRGCEYDALLPWPFQKV 494  
 DB 1804 -----FKTRNREMEVL--DSFRQOV 1822  
 RESULT 14  
 ID GCG4 HUMAN STANDARD; PRT; 2230 AA.  
 AC Q13439; Q14436; Q13270; Q13654;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Golgi autoantigen, golgin subfamily A 4 (Trans-Golgi p230) (256 kDa  
 DE golgin) (Golgin-245) (72.1 protein).  
 CN GOLG4.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING.  
 RX MEDLINE=96215236; PubMed=8626529;  
 RA Erlich R., Gleeson P.A., Campbell P., Dietzsch E., Toh B.-H.;  
 RA "Molecular characterization of trans-Golgi p230: a human peripheral  
 RA membrane protein encoded by a gene on chromosome 6p12-22 contains  
 RA extensive coiled-coil alpha-helical domains and a granin motif."  
 RT J. Biol. Chem. 271:8328-8337(1996).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RA Seeliger H.P.;  
 RL Submitted (NOV-1994) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 131-2230 FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=96125112; PubMed=8537393;  
 RA Fritzler M.J., Lung C.-C., Hamel J.C., Griffith K.J., Chan E.K.L.;  
 RA "Molecular characterization of golgin-245, a novel Golgi complex  
 RA protein containing a granin signature."  
 RT J. Biol. Chem. 270:31262-31268(1995).  
 RL [4]  
 RP SEQUENCE OF 524-672 FROM N.A.  
 RC TISSUE=Gastric fundus;  
 RA Balague C.;  
 RL Thesis (1994), Instituto municipal de investigacion medica, Spain.  
 CC -!- FUNCTION: MAY PLAY A ROLE IN VESICULAR TRANSPORT FROM THE TRANS-  
 CC GOLGI  
 CC -!- SUBCELLULAR LOCATION: ASSOCIATED WITH THE CYTOPLASMIC FACE OF THE  
 CC GOLGI MEMBRANE.



FT CONFLICT 135 135 H -> Q (IN REF. 1).  
FT CONFLICT 185 185 T -> R (IN REF. 1).  
SQ SEQUENCE 1102 AA; 128008 MM; 2293668D049825DC CRC64;

## Query Match

4.9%: Score 146; DB 1; length 1102;

Best Local Similarity 21.4%; Pred. No 0.17; Matches 85; Conservative 69; Mismatches 143; Indels 100; Gaps 17;

QY 96 VKDVFVFNCKCKREI-LALQIYCENESRGCAGDITLGHLLVHLKNDCHFEELPCVPRDCK 154  
DB 695 VKKQVEDE--KSEVOLALE-----EAGALEHESKTLRFQL-----ELSQLKADFE 739  
QY 155 EKVLRKD-----LKDHYEKACKYREATC-SHCKSQVPMIALQKHEDTDCPCVYVSCPH-- 206  
DB 740 RKLAEKDEMONIRRNQRTIDSLQSTLDSEARSRNEAIRLKKMEGDLNEMETQLSHAN 799  
QY 207 -----KCSVOTLRSLS-----AHLSECYNAPSTCSFRRYGCVPFGTNOQIKA- 250  
DB 800 RHAAEATKSARGLOTQIK-ELQVOLDLGLHNEIDLKQLAVSDRRNN-LQSELDLRLAL 857  
QY 251 -----HEASSAVOHVNLKESWSNS-----LEKKVSLQNESVEKNKSIQSL 291  
DB 858 LDQTEBARAKLAHEHLEATERVNLHTQNTSLINQKKLEGDISQMONVEVESIQECRNA 917  
QY 292 HNOICSEIEIEROKEMLRNNESKILHQRVIDSOAEKELDKIIRPFQNMEEADSM- 350  
DB 918 EOKAKKAITDAMMAAEELKKEODTSAHLENNKKNNEQTIKDLQRL-----DEAEQIA 970  
QY 351 -----KSSVESLONRYTELES-----VKSAGQVARNITGLLESQLSRHDQMLSVH 395  
DB 971 LKGGKKQIQKLESRYRELENNLENNLRNSDAQGARRFERRIKELTYQSEDEKKNLA-- 1028  
QY 396 DIRLADMDFQVLETASYNGVLWIKIRDYKRRKQEA 432  
DB 1029 --RMQDLIDIKLQL-----KVKSYKHOAEAA 1051

Search completed: December 19, 2002, 14:54:48  
Job time : 19 secs

